

SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic
 Combinations Thereof

<130> SYN-128

<140> PCT/GB00/02457
 <141> 2000-06-23

<150> GB 9915215.9
 <151> 1999-06-29

<150> GB 9930536.9
 <151> 1999-12-23

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 33
 <212> PRT
 <213> Paecilomyces sp.

<220>
 <221> VARIANT
 <222> 1, 2
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> 1, 2
 <223> Xaa = Any Amino Acid

<400> 1
 Xaa Xaa Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
 1 5 10 15
 Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
 20 25 30
 Arg

<210> 2
 <211> 33
 <212> PRT
 <213> Paecilomyces sp.

<400> 2
 Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
 1 5 10 15
 Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
 20 25 30
 Arg

<210> 3
 <211> 35
 <212> PRT
 <213> Paecilomyces sp.

<220>
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 <222> 1, 2
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> 1, 2
 <223> Xaa = Any Amino Acid

<400> 3
 Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala
 1 5 10 15
 Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys
 20 25 30
 Val Cys Arg
 35

<210> 4
 <211> 332
 <212> DNA
 <213> Paecilomyces sp.

<400> 4
 ggcaagatct gcactcctgc tggagttgta cgtattttca tccatttcct ycaccactcc 60
 tctaacatga agcaactttc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120
 ccggacttcg ctgcacgggc ggcgtcaacg taagtcacca tggatctggc aagcgagacc 180
 ataacatgac gcagtatact aaccctggcc gttatagaac aaggttgtga gtcgacatgt 240
 tktacaacct ctacaaacgc gcgcactaat gacaacggta gtgccggtaa ttctagtgtc 300
 gcaacttttg agcgtgggat aagtatgctt cg 332

<210> 5
 <211> 320
 <212> DNA
 <213> Paecilomyces sp.

<400> 5
 gggaaaattt gtacgccggc gggggttgta cgtatttca tccatttcct ccaccactcc 60
 tctaacatga agcaactctc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120
 ccggacttcg ctgcacgggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
 aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
 acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
 cgtgggataa gtatgcttcg 320

<210> 6
 <211> 320
 <212> DNA
 <213> Paecilomyces sp.

<400> 6
 gggaaaatct gtacgccggc gggggttgta cgtattttca tccatttcct ccaccactcc 60

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tctaacaatga agcaactctc tcttctctct araaatgtcc cgcggtcttt ccttgctgcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
cgtgggataa gtatgcttcg                                     320

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<210> 7
 <211> 174
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide codon optimised

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<400> 7
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcccggc cgccctcccg 120
tgctgcccg gcctccgctg catcggcggc gtgaacaaca aggtgtgccg ctga      174

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<210> 8
 <211> 174
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic polynucleotide codon optimised

```

<400> 8
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggtaaaat ttgtaccccg gccggcgtga agtgcccggc cgccctcccg 120
tggtgtcccg gcctcagggtg tattggtggt gtgaataata aagtgtgtcg ctga      174

```

<210> 9
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence containing intron sequence

```

<400> 9
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcactcct gctggagttg tttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata actttttctaa tatatgacca aaacatgggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgcccccg acttcgctgc atcggcgggc tcaacaacaa ggtttgccgg 360
taa                                     363

```

<210> 10
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence

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<400> 10
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cctcctacgg caagatctgc actcctgctg gagttgtttg tttctgcttc 120
tacctttgat atatatataa taattatcat taattagtag taatataata tttcaaatat 180
ttttttcaaa ataaaagaat gtagtatata gcaattgctt ttctgtagtt tataagtgtg 240
tataatttaa tttataactt ttctaataata tgaccaaaac atggatgatgt ttagaaatgt 300
cccgcggctc ttctttgctg ccccggaactt cgctgcatcg gcggcggtcaa caacaagggtt 360
tgccggttaa
369

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```

<210> 11
<211> 363
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Synthetic sequence

```

```

<400> 11
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cctcctacat ctgcactcct gctggagttg ttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatgggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa
363

```

```

<210> 12
<211> 363
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Synthetic sequence containing intron and codon
      optimised

```

```

<400> 12
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcaccccg gccggcggtg ttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatgggtg atgttttagaa gtgcccggcc 300
gccctcccgt gctgccccgg cctccgctgc atcggcggcg tgaacaacaa ggtgtgccgc 360
tga
363

```

```

<210> 13
<211> 439
<212> DNA
<213> Paecilomyces sp.

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<400> 13
tctacttctt catctcacgc catatatcct cccaaaatca cacctcttcc ttcaccatgc 60
aaatctccgc cgtcattgtc gcaactcttcg ccagcgccgc catggccggc aagatctgca 120
ctcctgctgg agttgtacgt attttcatcc atttcctyca ccaactcctt aacatgaagc 180
aactttctct tctctctaga aatgtcccgc ggctcttcct tgctgccccg gacttcgctg 240
catcggcggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtatactaac cctggccgtt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaatc tagtgctgca acttttgagc 420

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gtgggataag tatgcttcg

439

<210> 14

<211> 102

<212> DNA

<213> Paecilomyces sp.

<400> 14

ggcaagatct gcactcctgc tggagttaaa tgtcccgcgg ctcttccttg ctgccccgga 60
 cttcgctgca tcggcggcgt caacaacaag gtttgccggt aa 102

<210> 15

<211> 84

<212> DNA

<213> Dahlia sp.

<400> 15

atggttaata gatctgttgc tttttctgct tttgttctta ttctttttgt tttggctatt 60
 tcagatattg cttctgtttc agga 84

<210> 16

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Radish signal sequence

<400> 16

atggctaagt ttgcttctat tattgctcct ttgtttgctg cacttgtttt gtttgctgca 60
 tttgaagctc caactatggt tgaagct 87

<210> 17

<211> 72

<212> DNA

<213> Zea mays

<400> 17

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
 gagatccagg cc 72

<210> 18

<211> 90

<212> DNA

<213> Nicotiana sp.

<400> 18

atgggatttg ttctcttttc acaattgcct tcattttctc ttgtctctac acttctctta 60
 ttctagtaa tatccactc ttgccgtgcc 90

<210> 19

<211> 51

<212> DNA

<213> Paecilomyces sp.

<400> 19

atgcaaactc ccgccgtcat tgtcgcactc ttgccagcg ccgccatggc c 51

<210> 20
 <211> 28
 <212> PRT
 <213> Dahlia sp.

<400> 20
 Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe
 1 5 10 15
 Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly
 20 25

<210> 21
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Radish protein target sequence

<400> 21
 Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val
 1 5 10 15
 Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala
 20 25

<210> 22
 <211> 24
 <212> PRT
 <213> Zea Mays

<400> 22
 Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val
 1 5 10 15
 Ser Leu Ala Val Glu Ile Gln Ala
 20

<210> 23
 <211> 30
 <212> PRT
 <213> Nicotiana sp.

<400> 23
 Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
 1 5 10 15
 Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
 20 25 30

<210> 24
 <211> 17
 <212> PRT
 <213> Paecilomyces sp.

<400> 24

Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met
 1 5 10 15
 Ala

<210> 25
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 25
 tcgggctcgc atgaattcgc ggccgcattt tttttttttt tttt 44

<210> 26
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 26
 tcgggctcgc atgaattcg 19

<210> 27
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 27
 atgaattcgc ggccgcat 18

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 28
 tcgggctcgc atgaattcgc g 21

<210> 29
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 29
 ctcgcatgaa ttgcgggccg c 21

 <210> 30
 <211> 17
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc feature
 <222> 9, 12, 15
 <223> n = A,T,C or G

 <221> misc feature
 <222> 9, 12, 15
 <223> n = A,T,C or G

 <400> 30
 athtgyacnc cngcngg 17

 <210> 31
 <211> 20
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc feature
 <222> 9, 12, 15, 18
 <223> n = A,T,C or G

 <221> misc feature
 <222> 9, 12, 15, 18
 <223> n = A,T,C or G

 <400> 31
 athtgyacnc cngcngngt 20

 <210> 32
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc feature
 <222> 3, 6, 9, 12, 15
 <223> n = A,T,C or G

 <221> misc feature
 <222> 3, 6, 9, 12, 15
 <223> n = A,T,C or G

<400> 32
 acnccngcng gngtnaa 17

 <210> 33
 <211> 17
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 3, 12, 15
 <223> n = A,T,C or G

 <221> misc_feature
 <222> 3, 12, 15
 <223> n = A,T,C or G

 <400> 33
 ccntgytgyc cnggnyt 17

 <210> 34
 <211> 16
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 2, 14
 <223> n = A,T,C or G

 <221> misc_feature
 <222> 2, 14
 <223> n = A,T,C or G

 <400> 34
 tnaartgyat hggngg 16

 <210> 35
 <211> 20
 <212> RNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 3, 6, 18
 <223> n = A,T,C or G

 <221> misc_feature
 <222> 3, 6, 18
 <223> n = A,T,C or G

<400> 35
 ggngtnaaya ayaargtntg 20

 <210> 36
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 12, 15, 18, 21, 24
 <223> n = inosine

 <400> 36
 aarathtgya cnccngcngg ngtnaa 26

 <210> 37
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 3, 6, 9, 12, 21, 24
 <223> n = inosine

 <400> 37
 ccngcnggng tnaartgycc ngcngc 26

 <210> 38
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 6, 9, 12, 15, 18
 <223> n = inosine

 <400> 38
 tgyccngcng cnytnccntg ytgycc 26

 <210> 39
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature

<222> 9, 12, 15
 <223> n = inosine

 <400> 39
 tgyathggng gngtnaayaa yaargt 26

 <210> 40
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 40
 taaatgtccc gcggtctttc c 21

 <210> 41
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 41
 cggtctttcc ttgctgcccc g 21

 <210> 42
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 42
 tgctgccccg gacttcgctg c 21

 <210> 43
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <221> misc feature
 <222> 23, 24, 25, 26, 27
 <223> n = A,T,C or G

 <221> misc feature
 <222> 23, 24, 25, 26, 27
 <223> n = A,T,C or G

 <400> 43
 ggtttaatta cccaagtttg agnnnnn 27

<210> 44
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 44
 ctcaaacttg ggtaattaaa cc 22

<210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 45
 ggtttaatta cccaagtt 18

<210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 46
 taattaccca agtttgag 18

<210> 47
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 47
 ggtttaatta cccaagtttg ag 22

<210> 48
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<221> misc_feature
 <222> 3, 15, 18, 21
 <223> n = inosine

<400> 48

canacyttrt trttnacncc ncc 23

<210> 49
 <211> 21
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 <213> Artificial Sequence

<220>
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<400> 49
 atgcagcgaa gtccggggca g 21

<210> 50
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 50
 ggggcagcaa ggaagagccg c 21

<210> 51
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 51
 aagagccgcg ggacatttaa c 21

<210> 52
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 52
 agttaaatgt cccgcggctc ttccttgctg ccccggaatt cgctgcac 49

<210> 53
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 53
 gatgcagcga agtccggg 18

<210> 54
 <211> 718
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PROTEIN crylIal Embl. Accession No. X62821

<221> VARIANT
 <222> 602
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> 602
 <223> Xaa = Any Amino Acid

<400> 54
 Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320

```

Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
      325      330      335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
      340      345      350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
      355      360      365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
      370      375      380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385      390      395      400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
      405      410      415
Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile Ala
      420      425      430
Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln Leu
      435      440      445
Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro Asn
      450      455      460
Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser Ala
465      470      475      480
Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala Asp
      485      490      495
Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu Val
      500      505      510
Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro Gly
      515      520      525
Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
      530      535      540
Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg Val
545      550      555      560
Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser Ile
      565      570      575
Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn Arg
      580      585      590
Gly Glu Asp Leu Asp Tyr Lys Thr Phe Xaa Thr Val Gly Phe Thr Thr
      595      600      605
Pro Phe Ser Leu Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala Trp
      610      615      620
Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val
625      630      635      640
Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala Gln
      645      650      655
Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu Lys
      660      665      670
Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu
      675      680      685
Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe Glu
      690      695      700
Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
705      710      715

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<210> 55

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia2 Embl. Accession No. M98544

<400> 55

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Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1           5           10           15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
          20           25           30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
          35           40           45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
          50           55           60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65           70           75           80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
          85           90           95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
          100          105          110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
          115          120          125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
          130          135          140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145          150          155          160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
          165          170          175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
          180          185          190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
          195          200          205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
          210          215          220
Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
225          230          235          240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
          245          250          255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
          260          265          270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
          275          280          285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
          290          295          300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305          310          315          320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
          325          330          335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
          340          345          350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
          355          360          365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
          370          375          380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385          390          395          400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
          405          410          415
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile

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			420					425				430			
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln
		435					440					445			